

CHRONIC KIDNEY DISEASE STAGE IDENTIFICATION IN HIV INFECTED PATIENTS USING SUPERVISED MACHINE LEARNING: A REVIEW

Er. Rishabh Aryan

M.Tech (Artificial Intelligence and Data Science),
Department of Computer Science and Engineering,
Indian Institute of Information Technology, Bhagalpur (Bihar)
E-mail: rishabh.250201011@iiitbh.ac.in

Abstract — Chronic Kidney Disease (CKD) represents a major global health burden, particularly among individuals infected with Human Immunodeficiency Virus (HIV). The co-existence of HIV and CKD dramatically accelerates renal deterioration, making early and accurate detection essential for timely clinical intervention. Conventional diagnostic pathways often fail to identify CKD in its subclinical phases because the disease is largely asymptomatic until advanced stages. The emergence of supervised machine learning (ML) has provided a transformative opportunity to automate and enhance the classification of CKD stages, reducing diagnostic latency and improving prognostic accuracy. This review paper critically synthesizes published research on the application of supervised ML algorithms—including Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree (DT), Random Forest (RF), AdaBoost, XGBoost, and deep neural networks (DNN)—for the identification of CKD stages in HIV-infected patients. The role of the estimated Glomerular Filtration Rate (eGFR) in demarcating the five clinical stages of CKD is examined alongside feature-selection strategies such as Recursive Feature Elimination (RFE). Comparative performance metrics—accuracy, precision, and recall—are tabulated across studies to highlight methodological advances and existing research gaps. The review concludes that DNN consistently outperforms classical ML classifiers, achieving up to 99% accuracy, and advocates for future research that integrates multi-modal medical imaging with feature-based deep learning for robust clinical decision support.

Index Terms — *Chronic Kidney Disease; HIV; Supervised Machine Learning; Support Vector Machine; Deep Neural Network; eGFR; CKD Stage Identification; Feature Selection; KNN; Random Forest.*

I. INTRODUCTION

Chronic kidney disease is a persistent and progressive deterioration of renal function that poses one of the most formidable challenges in contemporary global healthcare. CKD is characterized by a gradual decline in the glomerular filtration rate (GFR), the metabolic efficiency by which the kidneys filter blood. When kidney function falls below critical thresholds, toxic metabolites accumulate in the bloodstream, precipitating a cascade of systemic complications, including cardiovascular disease, metabolic acidosis, anemia, and mineral-bone disorder [1]. Globally, CKD affects an estimated 700 million individuals, with disproportionate representation in low-income and middle-income countries where access to renal replacement therapy remains severely constrained [2].

The clinical burden of CKD is substantially compounded in patients living with HIV. Antiretroviral therapy (ART), while life-extending, can itself exert nephrotoxic effects on proximal tubular cells, particularly through agents such as tenofovir disoproxil fumarate [1]. Furthermore, HIV-associated

Nephropathy (HIVAN)—a collapsing form of focal segmental glomerulosclerosis—can rapidly progress to end-stage renal disease in genetically susceptible individuals, particularly those of African descent [3]. The interplay between viral-mediated glomerular injury, medication toxicity, and conventional CKD risk factors such as hypertension and diabetes creates a clinically complex phenotype that demands sophisticated diagnostic tools.

A fundamental obstacle to effective management is the absence of overt symptoms during the early and intermediate stages of CKD. Patients are frequently unaware of their condition until irreversible nephron loss has occurred, at which point dialysis or transplantation are the only viable interventions [4]. Automated, data-driven diagnostic models offer a promising solution by leveraging routinely collected laboratory and demographic data to classify patients into CKD stages before clinical manifestation. The availability of curated pathology datasets—most notably the University of California, Irvine (UCI) Machine Learning Repository CKD dataset—has catalyzed a proliferation of ML-based classification studies [5].

Supervised machine learning encompasses a broad family of algorithms that learn discriminative patterns from labeled training data to generalize predictions to unseen instances. In the context of CKD, classifiers are trained on patient records annotated with confirmed CKD diagnoses and severity stages, enabling them to predict the renal status of new patients from their laboratory profiles. This review examines the landscape of supervised ML research applied to CKD stage identification in HIV-infected patients, evaluates the performance of prominent algorithms, and identifies directions for future inquiry.

II. RELATED WORK

The intersection of HIV management and CKD detection has attracted considerable research attention over the past decade. Bagnis et al. [1] conducted a comprehensive clinical review documenting that angiotensin-converting enzyme (ACE) inhibitors and angiotensin receptor blockers (ARBs) significantly decelerate CKD progression in HIV-positive individuals, particularly those presenting with proteinuria. Their work underscored the necessity of early biochemical screening as a cornerstone of HIV renal care, yet did not employ computational classification methods.

Liu et al. [2] developed an integrated ML framework for CKD diagnosis that combined multiple imputation techniques to handle missing clinical values with KNN-based classification. Their model demonstrated satisfactory accuracy on the standard UCI CKD dataset and highlighted data quality as a critical determinant of model performance. Anwar and Rady [3] extended this work by evaluating Probabilistic Neural Networks (PNN), SVM, and Multilayer Perceptron (MLP) on 361 confirmed CKD patients. Their findings suggested that PNN produced the most stable predictions across a range of clinical scenarios, potentially owing to its non-parametric density estimation framework.

Amin et al. [4] contributed a rigorous methodological investigation into the impact of class imbalance on CKD classification. By comparing model performance on original imbalanced data against synthetically balanced datasets, they demonstrated that feed-forward neural networks achieved a recall of 0.99 and an F1-score of 0.99, markedly outperforming logistic regression baselines. Vaisla et al. [5] addressed the high dimensionality of CKD datasets through attribute evaluation, reducing features from 25 to as few as 6 without significant accuracy degradation, providing evidence that parsimonious feature sets can sustain predictive performance.

Perumal and Arulanthu [6] conducted a multi-classifier comparison on clinical CKD data using JRip, Sequential Minimal Optimization (SMO), and Naïve Bayes, concluding that the JRip rule-based learner produced the best overall performance. Manickam et al. [7] introduced Ant Lion Optimisation (ALO) as a meta-heuristic feature selector coupled with deep neural networks, demonstrating that evolutionary feature search can substantially improve classification accuracy beyond what conventional filter or wrapper methods achieve. Shinde et al. [8] combined ML-based CKD prediction with a personalized dietary recommendation system anchored on blood potassium levels, illustrating the translational potential of ML models in clinical practice. Collectively, these studies form the evidence base upon which the present review synthesises findings specific to the HIV-CKD context.

Table 1: Summary of Related Literature on CKD Stage Identification using Machine Learning

Ref.	Authors & Year	Methodology	Dataset	Key Finding
[1]	Bagnis et al. (2020)	Clinical analysis of HIV-CKD linkage	HIV patient cohort	ACE inhibitors slow CKD progression in HIV
[2]	Liu et al. (2020)	KNN with data imputation	UCI CKD	Sufficient accuracy with integrated model
[3]	Anwar & Rady (2019)	PNN, SVM, MLP	361 CKD patients	PNN best for stage identification
[4]	Amin et al. (2019)	Logistic Regression, FFNN	Real + oversampled	FFNN: 0.99 F1 score
[5]	Vaisla et al. (2016)	Attribute selection + classifiers	UCI CKD	Features reduced from 25 to 6–12
[6]	Perumal et al. (2019)	JRip, SMO, Naïve Bayes	Clinical data	JRip generates best performance
[7]	Manickam et al. (2018)	ALO + DNN	UCI CKD	ALO improves DNN accuracy
[8]	Shinde et al. (2019)	ML + diet recommendation	CKD dataset	Potassium zone-based diet plans
[9]	Yadav & Jat (2020)	Feature selection + dimensionality reduction	Chronic disease data	PCA + RF optimal
[10]	Darveshwala et al. (2021)	SVM, KNN, DT, RF, AdaBoost, XGBoost, DNN	UCI HIV-CKD (158 instances)	DNN: 99% accuracy with eGFR staging

Source: Compiled by authors from reviewed literature [1–10]

III. METHODOLOGY

A. Dataset Description

The primary experimental dataset referenced in the most comprehensive study under review [10] was sourced from the UCI Machine Learning Repository. It contains 158 patient records specific to the HIV-CKD population, with 27 attributes encompassing numerical and categorical clinical measurements as detailed in Table 2. This dataset is particularly valuable because it extends the widely used general CKD

dataset with HIV-specific demographic and pathological variables, enabling targeted analysis of renal complications in immunocompromised patients.

Table 2: Attributes of the HIV-CKD Patient Dataset [10]

No.	Feature	Data Type	Description
1	Age	Numerical	Patient age in years
2	Gender	Categorical	Male / Female
3	Ethnicity	Numerical	Encoded ethnic group
4	Blood Pressure	Numerical	Systolic blood pressure (mmHg)
5	Specific Gravity	Numerical	Urine specific gravity
6	Albumin	Numerical	Albumin level in urine
7	Sugar	Numerical	Urine sugar concentration
8	Red Blood Cells	Numerical	RBC count in urine
9	Pus Cell	Numerical	Pus cell count in urine
10	Pus Cell Clumps	Numerical	Clump presence in urine
11	Bacteria	Numerical	Bacterial count
12	Blood Glucose Random	Numerical	Random blood glucose (mg/dL)
13	Blood Urea	Numerical	Blood urea nitrogen (mg/dL)
14	Serum Creatinine	Numerical	Serum creatinine (mg/dL)
15	Sodium	Numerical	Serum sodium (mEq/L)
16	Potassium	Numerical	Serum potassium (mEq/L)
17	Haemoglobin	Numerical	Haemoglobin level (g/dL)
18	Packed Cell Volume	Numerical	Haematocrit (%)
19	White Blood Cell Count	Numerical	WBC count (cells/cumm)
20	Red Blood Cell Count	Numerical	RBC count (millions/cumm)
21	Hypertension	Numerical	Yes=1 / No=0
22	Diabetes Mellitus	Categorical	Yes / No
23	Coronary Artery Disease	Categorical	Yes / No
24	Appetite	Categorical	Good / Poor
25	Pedal Edema	Categorical	Yes / No
26	Anaemia	Categorical	Yes / No
27	Class	Categorical	CKD / Not CKD

Source: Darveshwala et al. [10], UCI Machine Learning Repository

B. Data Preprocessing

Clinical datasets invariably contain missing values, outliers, and categorical variables requiring encoding before ML models can be applied. Standard preprocessing steps include mean imputation for missing numerical values, mode imputation for categorical variables, and label encoding or one-hot encoding for nominal features such as diabetes mellitus status and appetite [4]. Normalization using min-

max scaling ensures that features with large numerical ranges, such as white blood cell count, do not dominate distance-based classifiers like KNN.

Recursive Feature Elimination (RFE) was employed in the core study [10] as a wrapper-based attribute selection strategy. By iteratively training a model and pruning the least important feature at each step, RFE reduced the 27-attribute space to 14 informative predictors. This dimensionality reduction not only mitigates overfitting but also improves computational efficiency and model interpretability—crucial considerations for clinical deployment where transparent reasoning is valued by healthcare professionals [5].

C. Supervised ML Classifiers Reviewed

Support Vector Machine (SVM): SVM constructs a maximum-margin hyperplane in a transformed feature space to separate classes. The choice of kernel function—linear, polynomial, or radial basis function (RBF)—determines how non-linearly separable data is handled. In CKD classification, SVM demonstrated 93% accuracy with 14 RFE-selected features [10], though it underperformed relative to ensemble and deep learning approaches, partly due to sensitivity to feature scaling and kernel parameterization [3].

K-Nearest Neighbors (KNN): KNN classifies an instance by majority vote among its k closest training samples in the feature space. Its non-parametric nature makes it robust to distributional assumptions, though it is computationally expensive at inference time on large datasets. KNN achieved 97% accuracy in the reviewed study [10], confirming earlier findings by Liu et al. [2] that appropriate imputation strategies enable KNN to handle clinical data effectively.

Decision Tree (DT): Decision trees recursively partition the feature space based on information gain or Gini impurity. Although interpretable, individual trees are prone to overfitting, particularly in small datasets such as the 158-instance HIV-CKD cohort [5]. DT achieved 97% accuracy; however, its precision (96%) slightly lagged behind ensemble variants, consistent with known limitations of single-tree classifiers in medical applications [8].

Random Forest (RF): Random Forest mitigates the variance of single decision trees by constructing an ensemble of decorrelated trees trained on bootstrapped subsets of training data and random feature subsets. This bagging strategy yields robust out-of-bag estimates and feature importances, making RF both a competitive classifier and a diagnostic tool for identifying clinically relevant biomarkers [7]. RF achieved 95% accuracy on the CKD-HIV dataset.

Gradient Boosting Variants (AdaBoost and XGBoost): Boosting algorithms sequentially train weak learners, with each subsequent learner focusing on misclassified instances from the prior iteration. AdaBoost re-weights training samples, while XGBoost employs gradient descent in function space with regularization terms that prevent overfitting. Both achieved 97% accuracy in the reviewed study [10], with AdaBoost demonstrating particularly strong recall (97%), a critical metric in medical screening where false negatives carry high clinical cost.

Deep Neural Network (DNN): The DNN architecture implemented in the primary study [10] employed all 24 biological attributes (excluding the target class) across multiple fully connected hidden layers with non-linear activation functions. Unlike classical ML classifiers that utilized 14 RFE-selected features, the DNN's hierarchical representation learning enabled it to extract informative composite features automatically. The model achieved 99% accuracy, 99% precision, and 98% recall—the highest

performance across all classifiers—supporting the growing consensus that deep architectures excel in high-dimensional biomedical classification tasks [4, 7].

IV. CKD STAGE IDENTIFICATION USING EGFR

The clinical severity of CKD is internationally stratified into five stages based on the estimated Glomerular Filtration Rate (eGFR), a composite indicator of renal filtration capacity computed from serum creatinine, age, sex, and ethnicity [17]. The Modification of Diet in Renal Disease (MDRD) equation used in the reviewed studies is expressed as follows:

$$\text{eGFR} = 175 \times (\text{Creatinine} / 88.4)^{-1.154} \times (\text{Age})^{-0.203} \times (0.742 \text{ if female}) \times (1.210 \text{ if Black ethnicity})$$

This formula operationalizes the eGFR as a continuous index that is subsequently discretized into six clinically defined stages as tabulated in Table 3 below. In the HIV context, nephrotoxic antiretroviral agents and viral-mediated glomerular injury can precipitate rapid progression between stages, necessitating frequent monitoring and accurate staging to guide therapeutic decisions [1].

Table 3: Clinical Stages of Chronic Kidney Disease Based on eGFR [17]

Stage	Clinical Description	eGFR Range (mL/min/1.73m ²)	HIV Risk Level
Stage 1	Normal kidney function with evidence of damage	> 90	Moderate
Stage 2	Mildly reduced kidney function	60 – 89	Moderate
Stage 3A	Mildly to moderately reduced	45 – 59	High
Stage 3B	Moderately to severely reduced	30 – 44	High
Stage 4	Severely reduced kidney function	15 – 29	Very High
Stage 5	Kidney failure / End-Stage Renal Disease	< 15	Critical

Source: National Kidney Foundation, KDIGO Clinical Practice Guidelines [17]

Among the 158 HIV-CKD patient instances studied by Darveshwala et al. [10], 44 patients were confirmed CKD-positive following ML classification. The eGFR-based stage distribution of these 44 patients is presented in Table 4, revealing a pronounced concentration in the advanced stages: 25 of 44 patients (56.8 %) had progressed to Stage 5, underscoring the severity of HIV-associated renal disease and the critical need for earlier detection interventions.

Table 4: Distribution of HIV-CKD Patients Across Disease Stages [10]

Stage	Stage 1	Stage 2	Stage 3A	Stage 3B	Stage 4	Stage 5
No. of Patients	1	1	2	5	10	25

Source: Darveshwala et al. [10]

V. RESULTS AND COMPARATIVE ANALYSIS

Table 5 presents the consolidated performance metrics of all supervised ML classifiers evaluated in the primary study [10], enabling direct algorithmic comparison. Three standard evaluation measures are reported: accuracy (the proportion of all predictions that are correct), precision (the proportion of positive predictions that are true positives), and recall (the proportion of actual positive cases correctly identified).

In clinical applications, high recall is prioritized to minimize missed diagnoses of CKD in HIV-positive patients.

Table 5: Comparative Performance of Supervised ML Classifiers for CKD-HIV Classification [10]

Classifier	Accuracy (%)	Precision (%)	Recall (%)	Attributes Used
SVM	93	91	92	14 (RFE selected)
KNN	97	95	96	14 (RFE selected)
Decision Tree	97	96	96	14 (RFE selected)
Random Forest	95	95	94	14 (RFE selected)
AdaBoost	97	96	97	14 (RFE selected)
XGBoost	97	95	96	14 (RFE selected)
DNN	99	99	98	24 (all features)

Source: Darveshwala et al. [10]; Note: DNN trained on all 24 attributes; others on 14 RFE-selected features

The results unambiguously position DNN as the superior classifier, achieving 99% across accuracy and precision metrics and 98% recall. Among classical ML algorithms, KNN, Decision Tree, AdaBoost, and XGBoost achieved parity at 97% accuracy, while Random Forest attained 95% and SVM demonstrated the lowest performance at 93%. The inferior SVM performance is consistent with findings from Anwar and Rady [3], who observed that SVM's sensitivity to kernel selection and its convex optimization assumption can reduce robustness when datasets contain overlapping class boundaries—a characteristic feature of early-stage CKD presentations.

The DNN's superior performance despite relying on all 24 features rather than the 14-feature reduced set further demonstrates the capacity of deep architectures to independently perform implicit feature selection through weight regularization and dropout mechanisms. This finding aligns with Manickam et al. [7], who demonstrated that optimization-guided feature selection coupled with deep learning consistently outperforms shallow classifiers irrespective of feature set size.

VI. DISCUSSION

A. Clinical Significance

The clinical implications of automated CKD staging in HIV-infected patients extend well beyond diagnostic convenience. Early-stage identification (Stages 1–2) enables clinicians to modify nephrotoxic ART regimens, intensify blood pressure management, and introduce dietary modifications that collectively delay progression to end-stage renal disease [1, 8]. Late-stage patients (Stages 4–5) require immediate preparation for renal replacement therapy, and accurate automated staging can streamline referral pathways in resource-constrained settings where nephrologists are scarce [2].

B. Limitations of Existing Studies

Several methodological limitations are observed across the reviewed literature. First, most studies employed the standard UCI CKD dataset or closely related derivatives, which contain fewer than 400 instances. Small sample sizes inflate variance in performance estimates and limit the statistical power needed to detect subtle inter-stage differences. Second, class imbalance—wherein non-CKD instances substantially outnumber CKD cases—was not consistently addressed. Amin et al. [4] demonstrated that

oversampling substantially improves recall, yet subsequent studies have not uniformly adopted this practice.

Third, cross-study comparisons are complicated by heterogeneous preprocessing pipelines, feature sets, and validation strategies (holdout versus k-fold cross-validation).

C. Future Research Directions

Future investigations should prioritize prospective collection of HIV-CKD datasets from diverse geographic populations to improve generalizability. The integration of medical imaging modalities—renal ultrasound and magnetic resonance imaging—with structured pathology data offers a promising avenue for multi-modal DNN architectures that outperform unimodal models [10]. Explainability frameworks such as SHapley Additive exPlanations (SHAP) and Local Interpretable Model-Agnostic Explanations (LIME) should be applied to ML models intended for clinical deployment to satisfy emerging regulatory requirements for transparent algorithmic decision-making in healthcare. Finally, federated learning approaches could enable multi-institutional model training without compromising patient data privacy.

VII. CONCLUSION

This review has systematically examined supervised machine learning approaches for identifying chronic kidney disease stages in HIV-infected patients. The evidence synthesised from a decade of research demonstrates that ML classifiers offer accurate, scalable, and non-invasive alternatives to conventional CKD detection. Among the algorithms evaluated, deep neural networks consistently deliver superior classification performance, achieving up to 99% accuracy and 98% recall on HIV-CKD datasets. Classical ensemble methods—AdaBoost, XGBoost, and Random Forest—represent robust secondary options where computational resources limit DNN deployment.

The eGFR-based staging framework provides a clinically meaningful complement to binary CKD classification, enabling precise therapeutic stratification across the five disease stages. Given the disproportionate burden of CKD among HIV-positive populations and the critical importance of timely intervention, the adoption of validated ML pipelines in clinical renal screening programs represents a public health imperative. Future research should address dataset limitations, integrate multi-modal inputs, and develop explainable AI tools to facilitate translation of these computational advances into real-world clinical practice.

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